# Comparison of Bacterial Communities from 11 Soil Series in New York City

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Introduction

The profile characteristics of urban soils are likely to be disturbed by human activities and therefore there is a need to improve our understanding of their development and functioning. Microbial communities change due to anthropogenic disturbances and it is unclear how they respond along urban soil profiles. This study investigates the dynamic soil properties and the bacterial communities along the profiles of urban soils of New York City with varying degree of human disturbances.

Citywide (% of land area)	
Urban land	62.7
HAHTM Soils	27.6
NDM Soils	8.6
Other Misc. Areas	1.1
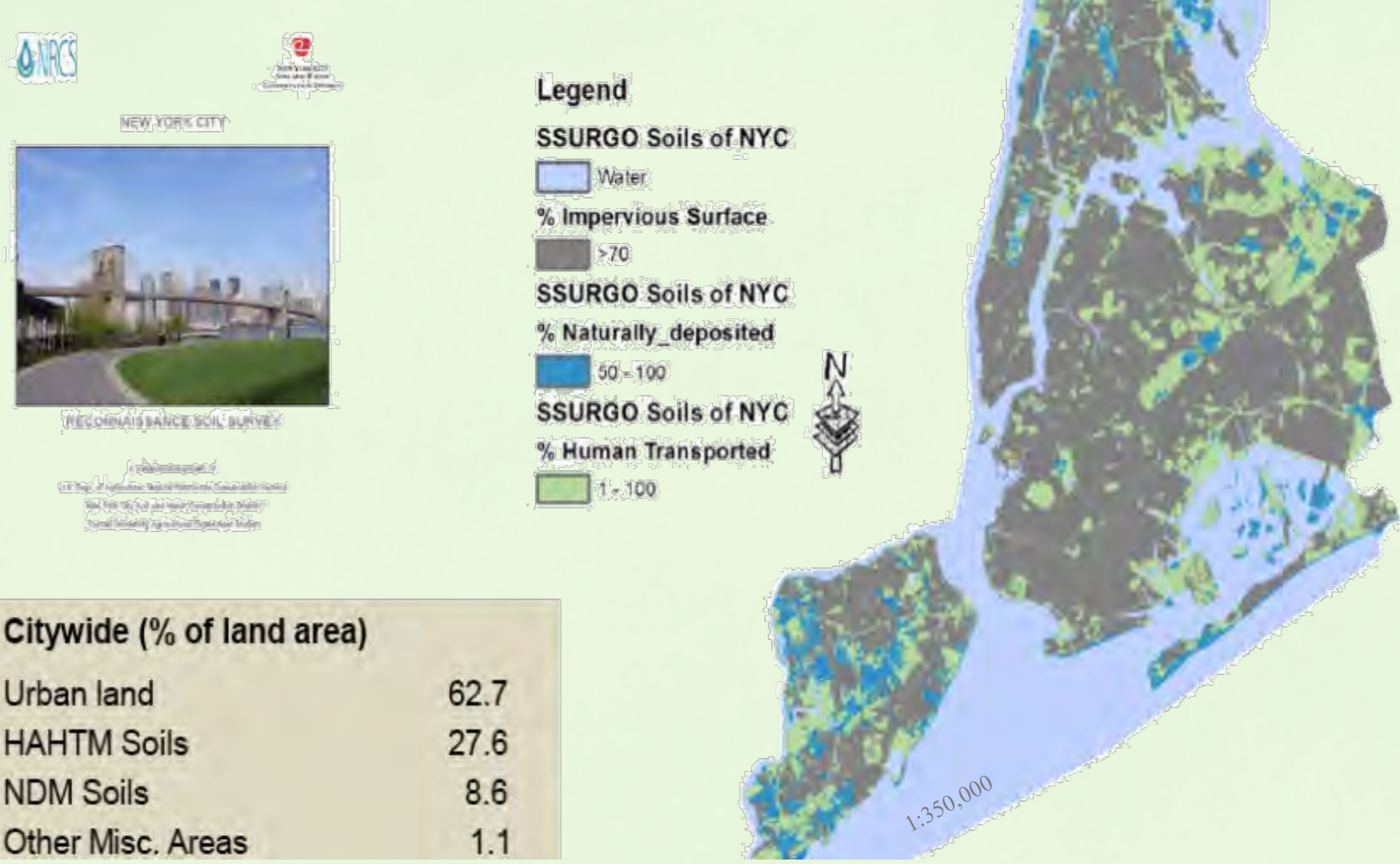
The **objective** of this work is to measure dynamic soil properties (DSPs) and examine microbial community composition along the continuum of urban soils across NYC.

Methods

❖ Sites were chosen to represent the diversity of previously described soil profiles around New York City and a reference soil in northern New Jersey. NYC soil included 5 with naturally deposited materials (NDM) and 5 with human transported materials (HAHTM).

▪ Four soils are formed in high artifact fill (>10% artifacts), such as construction debris (Laguardia and Secaucus series) or coal ash (Rikers and Mosholu series).

❖ Pedons (1m deep, unless bedrock or the water table were shallower) were described following USDA-NRCS criteria. At each horizon, soil samples were collected microbial (~10g) and soil (0.5-1kg) analyses. Soil analysis samples were air-dried and sieved at 2mm then the volumetric percentage of coarse natural and artifactual fragments was estimated.

❖ DNA was extracted from ~2g of soil using the MoBio PowerSoil kit. Bacterial communities were then molecularly identified using Illumina MiSeq sequencing (Mr. DNA, Shallowater, TX; V1-V3 & V4 regions of the 16S rRNA gene). Sequences were analyzed with QIIME and data was visualized with R. Taxonomy was assigned to operational taxonomic units (OTUs) using Greengenes.

❖ Characteristic pedon bacterial communities were determined by identifying OTUs present in ≥50% of the horizon samples and had more than 100 sequences/OTU. The Shannon-Weiner diversity index (H'; alpha diversity) was calculated and then converted to the 'effective number of species' (ENS; in this study species is considered as equivalent to OTU), which facilitates comparison across samples.

Acknowledgements

Results

❖ The soils formed in human-transported materials displayed a less differentiated profile and may have uneven distribution of organic matter and metals with depth. The most abundant bacterial taxa observed in these soils are also present in most natural and urban soils.

❖ **Characteristic bacteria of each soil series comprised 40% or more of the bacteria communities.** Bacteria taxa are differentiated by color representing the Phyla assignment then gradations of the Phyla color to indicate Order. Rockaway is the non-urban soil with urban soils separated into groups of naturally deposited material (NDM) and human associated and human transported material (HAHTM).
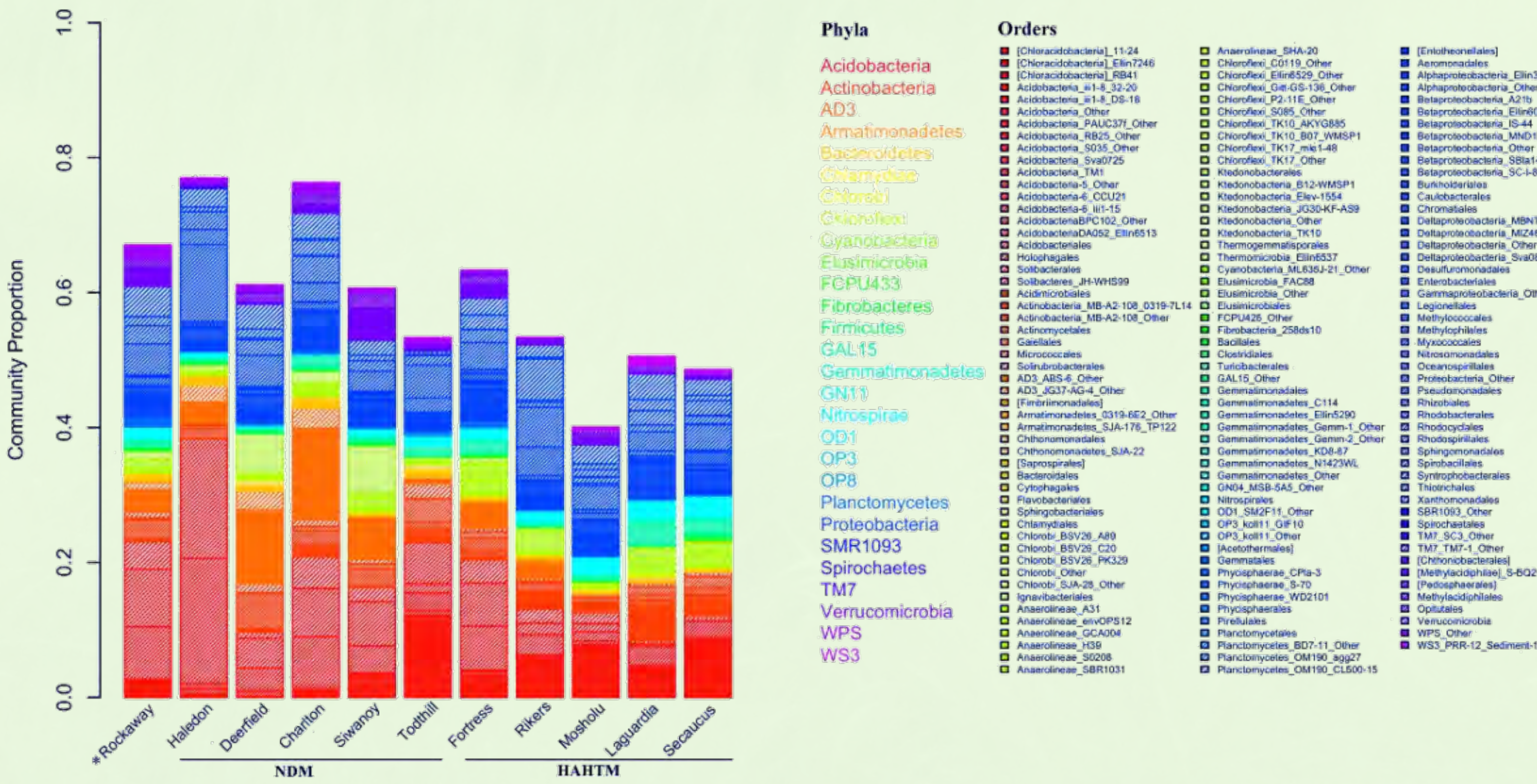
❖ **The relative abundance varied for the five most abundant bacterial orders along the soil profiles.** The heatmap represents the total abundance of the five most abundant (in average along the profile) identified bacterial orders relative to the remaining bacterial community.

❖ **Bacterial communities were incredibly diverse.** The human influenced samples had about the same species richness as the natural samples, however the composition and abundances contribute to a greater diversity.

Discussion

In these soil samples, the general bacterial communities are not different from the communities found in other soils. The bacterial diversity varied across the investigated soils and was lower in some soils formed in naturally deposited materials displaying marked variations of the community structure along their profiles. The changes in bacterial community composition depending on the soil horizons were less pronounced in less differentiated soils, such as the soils formed in human-transported materials or in weathered soils with relatively stable distribution of soil properties along their profiles. This suggests that potential links exist between human activities, soil development, dynamic soil properties and bacterial community composition in NYC soils. However, further data analyses are required to better understand which soil properties are driving the microbial diversity in these soils. The influence of human activities on soil development and functioning in relation to the microbial diversity needs to be investigated across a wider range of urban soils.